IN THE CLAIMS

1. (Currently amended) A method of identifying a compound that binds to a coactivator binding site of a nuclear receptor, said method comprising:

modeling a test ~~compounds~~ compound that ~~fit~~ fits spatially into the nuclear receptor coactivator binding site using an atomic structural model of the nuclear receptor coactivator binding site or portion thereof; and

screening said test ~~compounds~~ compound in an assay that measures binding of a test compound to the nuclear receptor coactivator binding site, thereby identifying a test compound that binds to the coactivator binding site of said nuclear receptor.

2. (Currently amended) The method of claim 1, wherein said atomic structural model comprises atomic coordinates of amino acid residues identified by homology alignment with residues of a portion of human thyroid beta receptor, [[()]represented as SEQ ID NO: 52 or as SEQ ID NO: 53[()]], selected from the group consisting of Val284, Phe293, Ile302, Leu305, and Leu454.

44. (New) The method of claim 1, wherein the atomic structural model comprises the set of structure coordinates depicted in Appendix 1, or a homologue thereof, the homologue having a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å.

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45. (New) The method of claim 1 wherein the atomic structural model is experimentally derived.

46. (New) The method of claim 1, wherein said atomic structural model additionally comprises atomic coordinates of a molecule bound to the coactivator binding site.

47. (New) The method of claim 46 wherein the molecule is a peptide.

48. (New) The method of claim 47 wherein the peptide comprises a nuclear receptor box sequence.

49. (New) The method of claim 48 wherein the peptide comprises a GRIP1-nuclear receptor box 2 sequence given by SEQ ID NO: 6.

50. (New) The method of any one of claims 2 to 8 wherein the test compound interacts with at least one of the amino acid residues.